UNITED STATES DISTRICT COURT
SOUTHERN DISTRICT OF NEW YORK

UNITED STATES OF AMERICA,	:	
- v. -	:	S1 17 Cr. 438 (VEC)
EDWIN CORTORREAL a/k/a "Crazy Ed,"	:	
Defendant.	:	

THE GOVERNMENT'S OPPOSITION TO DEFENDANT'S MOTION TO EXCLUDE DNA EVIDENCE FROM A ROLL OF DUCT TAPE AND FOR A *DAUBERT* HEARING

AUDREY STRAUSS
United States Attorney for the
Southern District of New York
One St. Andrew's Plaza
New York, NY 10007

Courtney Heavey
Adam Hobson
Justin Rodriguez
Assistant United States Attorneys
- *Of Counsel* -

TABLE OF CONTENTS

PRELIMINARY STATEMENT

The Government respectfully submits this Opposition to the Defendant's Motion to Exclude DNA Evidence from a Roll of Duct Tape and Request for a *Daubert* Hearing (the "Motion") (ECF Doc. 636). For the reasons stated in this Opposition, that Motion should be denied without holding a *Daubert* hearing.

Count Two of the superseding indictment charges Defendant Edwin Cortorreal with murder in aid of racketeering in connection with a robbery that Cortorreal and his co-conspirators committed, during which Cortorreal shot the victim in the head and killed him. Two types of DNA evidence link the defendant in this case to the charged crime: 1) DNA from a cellphone battery found in the stairwell of the victim's apartment, and 2) DNA from a roll of duct tape from the victim's apartment. OCME used its Low-Copy Number ("LCN") testing protocols to amplify and examine both pieces of DNA evidence. Defendant's *Daubert* motion concerns only the DNA analysis of the duct tape.

OCME concluded that the duct tape sample was a mixture with at least three contributors, that the defendant was included as a possible contributor, and using its Forensic Statistical Tool ("FST") program, calculated a likelihood ratio showing that it "is approximately 11,400 times more probable if the sample originated from Edwin Cortorreal and two unknown, unrelated persons, than if it originated from three unknown, unrelated persons." Silverman Ex. A at Cortorreal_000031.[1] Because the likelihood ratio was over 1,000, OCME further concluded that there was "very strong support" that Cortorreal was a possible contributor, the strongest qualitative standard under the OCME's FST protocol.

[1] Citations to "Silverman Ex." refer to the exhibits to the declaration of Benjamin Silverman, which was filed in connection with the defendant's present motion and is available at docket number 637. Citations to "Br." refer to the memorandum of law defendant submitted in connection with the present motion, which is available at docket number 636.

The defendant moves to preclude the DNA evidence from the roll of duct tape under Federal Rule of Evidence 702 and *Daubert* v. *Merrell Dow*, 509 U.S. 579 (1993). Defendant raises five challenges: 1) that OCME incorrectly concluded that the mixture contained three or more contributors, when the mixture contained at least four contributors; 2) OCME's conclusion that there is "very strong" support that defendant contributed to the mixture is arbitrary, and other labs use a different verbal scale; 3) OCME intentionally diluted the sample to avoid using High-Copy Number ("HCN") testing protocols, and LCN testing is controversial and unreliable; 4) a change in FST's source code caused FST to disregard DNA information and likely produced more inculpatory results; and 5) FST does not comply with software engineering standards.

The vast majority of these arguments were raised and rejected in *United States v. Morgan*, 53 F. Supp. 3d 732 (S.D.N.Y. 2014), which challenged LCN testing, and *United States v. Jones*, 2018 WL 2684101 (S.D.N.Y. June 5, 2018), which challenged FST. In both *Morgan* and *Jones*, the district court considered multiple rounds of briefing, conducted multi-day *Daubert* hearings, and held that, at best, defendant's arguments went to the weight, not admissibility of the evidence. In both cases the Second Circuit affirmed.

Defendant does not claim that *Morgan* or *Jones* were incorrectly decided and fails to identify any reason for reaching a different result in this case. In fact, the only new argument raised is that OCME intentionally diluted the sample to avoid using HCN testing, which is factually flawed, and not a basis for exclusion given that, as confirmed in *Morgan*, LCN is a valid and reliable testing process. Defendant also cites two 2019 articles regarding FST, but these materials are further evidence that researchers have analyzed FST and have not identified any issue that undermines its reliability. At best, defendant's arguments go to the weight and not the admissibility of the evidence and thus defendant's motion should be denied.

BACKGROUND

I. The Relevant Evidence at Trial

The Government expects that the evidence at trial will show that Edwin Cortorreal was a member of a violent organization known as the "Hot Boyz." On October 27, 2006, Cortorreal and several other Hot Boyz members used a hydraulic pump to break into the apartment of a wholesale marijuana trafficker, Kelly Diaz. Cortorreal and his co-conspirators carried guns and assaulted Kelly Diaz and his girlfriend. While other co-conspirators ransacked the apartment, Cortorreal forced Diaz and Diaz's girlfriend to the floor. Cortorreal and Diaz exchanged hostile words and Cortorreal then fired a single shot into Diaz's head at close range, killing him and leaving Diaz's girlfriend trapped under Diaz's body. Cortorreal and his co-conspirators stole a large quantity of marijuana and cash and then fled before police arrived.

Law enforcement responding to Diaz's apartment recovered several items that were swabbed for DNA, including a cellphone battery found in the apartment stairwell, and a roll of duct tape found inside the apartment, which was used to restrain Diaz and his girlfriend. The swabs were sent to OCME for DNA analysis and OCME ran LCN testing on both swab 2B from the cellphone battery (the "Cellphone Battery Swab") and swab 1B from the roll of duct tape (the "Duct Tape Swab"). Because OCME concluded that the Duct Tape Swab was a mixture with at least three contributors, OMCE further used FST to calculate a likelihood ratio. The results of OCME's DNA analysis are described further below.

II. Basic Overview — DNA Analysis and OCME

A. Human DNA

Deoxyribonucleic acid ("DNA") is located in almost every cell of the human body; it contains all the information that determines an individual's genetic makeup. A DNA molecule consists of two strands that are coiled together in a ladder-like double helix. Each strand consists

of four bases. The base on one strand forms a "rung" of the ladder with a corresponding base on the other strand, and the order in which the base pairs are arranged constitutes an individual's DNA sequence. While about 99% of human DNA material is identical, no two people have the same DNA sequence, except for identical twins. *See, e.g.*, *United States* v. *Jakobetz*, 955 F.2d 786, 791-92 (2d Cir. 1992).

Modern DNA testing involves four basic steps: (1) extraction, (2) quantitation, (3) Polymerase Chain Reaction (or "PCR") amplification, and (4) analysis. *See United States v. Jones*, 965 F.3d 149, 155 (2d Cir. 2020). Extraction is the recovery of DNA from human cells. *Id.* Quantitation is the measurement of the amount of DNA extracted. *Id.* If enough DNA is detected, amplification can be done, wherein the DNA is copied multiple times to produce larger amounts of DNA. *Id.* Finally, the DNA is analyzed and compared to other DNA profiles.

Today, the most common method of DNA analysis involves short tandem repeat, or "STR." In STR analysis, scientists examine the number of times a sequence of bases repeats at a particular location (or "locus" or plural "loci") in a strand of DNA; this number constitutes the DNA type or "allele" present at that locus. *Maryland v. King*, 133 S. Ct. 1958, 1967-68 (2013); *see also United States v. Jones*, 2018 WL 2684101, at *2 (S.D.N.Y. June 5, 2018). For example, if ten repeats of a sequence of bases are present at a locus, the DNA allele would be "10." Because each person receives half of his DNA from one biological parent and half of his DNA from the other biological parent, each person generally has two DNA alleles at each locus.[2] *See Jones*, 2018 WL 2684101, at *2. Accordingly, the DNA type at one locus may be "10, 11," which is sometimes referred to as an "allele call," and would show the presence of ten STRs from one parent and eleven STRs from the other parent. *Id.* The resulting series of "allele calls"

[2] One exception is when an individual receives the same sequence of bases at a particular locus from both parents, which is called "homozygotes."

at the different loci constitutes the DNA profile, which can then be compared to other profiles to determine whether a DNA match exists. *Id*.

B. The Office of the Chief Medical Examiner's DNA Testing

The Office of the Chief Medical Examiner ("OCME") was established in 1918 and is the largest public forensic laboratory in the country; it is not affiliated with any law enforcement agency. *See Jones*, 965 F.3d at 155. DNA analysis at OCME is conducted by the Department of Forensic Biology, which has been performing DNA testing in criminal cases for three decades.[3] OCME's DNA analysis includes the examination of homicide, sexual assault, and other crime evidence for DNA extraction and typing, and that analysis may either incriminate or exclude a suspect.

OCME is accredited nationally by the ANSI-ASQ National Accreditation Board ("ANAB") under the American Society of Crime Lab Directors/Laboratory Accreditation Board International Program.[4] *See* Dr. O'Connor Decl. at ¶ 7. OCME is further accredited in New York by the State's Commission on Forensic Science ("NYS Commission"), which is comprised of leaders in the scientific and legal community. The NYS Commission is charged with "increase[ing] and maintain[ing] the effectiveness, efficiency, reliability, and accuracy of forensic laboratories, including forensic DNA laboratories," and "ensur[ing] that forensic analyses, including forensic DNA testing, are performed in accordance with the highest scientific standards practicable." *See* N.Y. Executive Law § 995-b (McKinney). Accordingly, the NYS Commission develops standards and a program of accreditation for all forensic laboratories in New York State.

---

[3] *See generally* https://www1.nyc.gov/site/ocme/about/about-ocme.page

[4] *See* https://anab.ansi.org/latest-news/anab-and-ascldlab-merge-operations (describing the merger of ANAB and ASCLD Lab).

As the Second Circuit noted, "[t]o maintain its accreditations, and to follow the quality assurance standards and guidelines established by the Scientific Working Group of DNA Analysis Methods ("SWGDAM,"), a group run by the Federal Bureau of Investigation ("FBI"), OCME is required to establish and adhere to certain protocols and standard operating procedures for every step of every procedure an analyst performs in the laboratory."[5] *Jones*, 965 F.3d at 155; *see also* Ex. A (*Morgan* Tr.) at 24-26 and Ex. B (*Jones* Tr.) at 12-15, 25 (Testimony of OCME's Dr. Craig O'Connor, discussing OCME's accreditations). To ensure OCME adheres to its protocols and procedures, OCME undergoes a detailed assessment every four years, annual surveillance by ANAB staff assessors, and biannual external audits. *See* Dr. O'Connor Decl. at ¶ 7. The auditors and assessors evaluate OCME's facilities and equipment, personnel, training, safety, the lab's compliance with standard operating procedures, validations for new equipment and technologies, and case file records and reports. *Id.* In the alternate years, OCME performs an internal audit and reports the results to both the FBI and ANAB. *Id.*

III. Low Copy Number ("LCN") DNA Testing

OCME historically performed two types of DNA testing: High Copy Number ("HCN") and Low Copy Number ("LCN"). Both HCN and LCN testing involve extraction, quantitation, PCR amplification, and analysis, but LCN was used for samples with lower amounts of DNA. *See United States v. Morgan*, 53 F. Supp. 3d 732, 736 (S.D.N.Y. 2014). The primary differences between HCN and LCN testing were the number of times the DNA was amplified, and the interpretation of those results. *Id.* For HCN, the DNA is amplified in 28 cycles of copying. *Id.* For LCN testing, the DNA was divided into three batches, and because a smaller amount of DNA was used, each batch was amplified 31 times through a more sensitive copying process,

[5] SWGDAM is a group of approximately 50 scientists representing federal, state and local forensic DNA laboratories in the United States and Canada. *See* http://swgdam.org

which was designed to identify and amplify more material. *See id.* Accordingly, LCN testing produced three results, one for each amplified batch. Analysts considered all the results and created a composite DNA profile based on all alleles present in two of the three batches. *See* STR Results Interpretation — Identifiler® and Yfiler®" (Effective March 9, 2018–December 30, 2020) (the "STR Results Interpretation Protocol") at 41.[6]

Beginning in 2003 and continuing for more than a year, OCME conducted extensive validation studies[7] that tested LCN's ability to reliably analyze DNA samples of different quantities and sources, as well as both single-source and mixture DNA samples. *See Morgan*, 53 F. Supp. 3d at 737-38. "As SWGDAM recommends, OCME used known samples in performing validation, so that it could verify its results." *Id*. at 738.

The small amount of starting DNA and the increased number of amplification cycles involved in LCN testing can increase stochastic effects, which are random errors in genetic testing. *See id.* at 736; Ex. A (*Morgan* Tr.) at 40-42. Stochastic effects include allelic drop-in, allelic drop-out, and stutter. *See* Ex. A (*Morgan* Tr.) at 42, 45-46.[8] OCME's extensive validation studies enabled OCME to develop protocols and interpretation guidelines to account

---

[6] Available at https://www1.nyc.gov/assets/ocme/downloads/pdf/technical-manuals/forensic-biology-technical-manuals/str_results_interpretation_identifiler_and_yfiler_030918.pdf. OCME's protocols are updated periodically and, accordingly, cited herein are the protocols in effect at the time of OCME's final report on the DNA analysis of the Duct Tape, dated April 16, 2020.

[7] Validation studies are the process through which the scientific community acquires the information necessary to determine the efficacy and reliability of a procedure. *See* Dr. O'Connor Decl. at ¶ 8; *Morgan*, 53 F. Supp. 3d at 737.

[8] Allelic drop-in occurs when an allele is detected that does *not* belong to a person or persons contributing to the sample. Allelic drop-out occurs when an allele that belongs to the person or persons contributing to the sample is not detected. Stutter sometimes occurs in the process of DNA replication, where alleles can become altered and create a small amount of a different allele that is then detected. *See Morgan*, 53 F. Supp. 3d at 736-37.

for the potential increase of stochastic effects. *See*, Ex. C (Theresa Caragine, *et al*., "Validation of Testing and Interpretation Protocols for Low Template DNA Samples Using AmpFlister® Identifiler®," Croatian Med. J., (2009) 250-67) ("Through extensive testing of low template single-source and mixed samples, we have developed quality control, testing, and interpretation protocols. These protocols were designed to address the concerns regarding the increased sensitivity of this system and the accompanying stochastic effects."); *see also Morgan*, 53 F. Supp. 3d at 738 ("Based on the results of these validation studies, OCME created its interpretation guidelines, intended to allow for consistent interpretation of LCN testing results by accounting for the presence of increased stochastic effects as the quantity of DNA decreases"); Ex. A (*Morgan* Tr.) at 38-41, 45-46, 77-78 (describing how LCN protocols take into account stochastic effects). OCME analysts used these protocols and interpretation guidelines in all LCN DNA testing.

The NYS Commission's DNA Subcommittee (the "DNA Subcommittee"), which is a group of "well-known and respected scientists and experts in the field of DNA analysis who advise [the NYS Commission] on matters relating to the implementation of scientific controls and quality assurance procedures for the performance of forensic DNA analysis,"[9] reviewed OCME's validation studies and program for LCN analysis. *See Morgan*, 53 F. Supp. 3d at 742 ("The studies were also examined and implicitly declared reliable by the Commission and its DNA Subcommittee, both comprised of leading experts in the field."). In 2005, the DNA Subcommittee issued a binding recommendation to the full Commission that OCME be approved to conduct LCN testing in forensic cases, and the full Commission approved. *Id.* at 739.

[9] *Jones*, 2018 WL 2684101, at *4.

IV. FST and DNA Testing on Mixtures

DNA samples containing one individual's DNA are single source, while samples containing multiple people's DNA are mixtures. *Jones*, 965 F.3d at 155. When analyzing mixtures, analysts use OCME protocols to estimate the number of contributors. Those protocols are tailored to HCN and LCN processes and consider a range of factors, including the number of alleles at each locus, and whether the alleles could be the result of stochastic effects. *See* STR Results Interpretation Protocol, at 20-24 (setting forth protocols for HCN); at 42-43 and 45-48 (setting forth protocols for LCN).

For LCN testing, OCME protocols provide that if the sample contains at least three repeating alleles in at least three loci, the sample must be considered a mixture. *Id.* at 42. The reason for this rule is that an individual generally has two alleles at any locus (one from each parent), and thus three or more alleles can signify more than one contributor. However, in samples where just one or two loci have three or more alleles and/or where the third allele did not repeat (*i.e.*, was only present in one of the batches), OCME's validation studies showed that the third "allele" was mostly likely a stochastic effect. Similarly, samples are considered three-person mixtures when there are at least five alleles at two or more loci in the composite.[10] *Id.* at 45. And samples are considered four or more person mixtures when there are seven or more alleles at two or more loci in the composite; such samples are labeled inconclusive. *Id.* at 42. The protocols further instruct that "[s]tutter and other explainable artifacts should be considered when counting the number of alleles at a locus." *Id.* at 45.

Once an analyst determines that the sample is a mixture with at least two or three contributors, the analyst determines whether one person's DNA predominates, such that the

[10] As stated above, an allele is only in the composite if it appears in at least two of the three batches.

analyst can identify a "major contributor." *Id.* at 43, 46-47. In such cases, analysts can treat the "major contributor" like a single source sample and use random match probability to determine whether the suspect's sample matches the sample collected from the evidence. This "major contributor" analysis is not possible, however, when the contributors to a mixture are too evenly balanced. In such instances, scientists compare the alleles in the evidence sample to the DNA profile of a suspect or victim. Based on that analysis, the scientist determines whether the person is included as a possible contributor to the evidence mixture. *See*, "Sample Comparisons – Identifiler® and YFiler®," (Effective July 19, 2019–Nov. 30, 2020) (hereinafter "Sample Comparisons Manual") at 4.[11]

A. A Scientific Consensus Develops That a Statistical Method is Needed, and OCME Develops FST

Before OCME developed and implemented FST, scientists were limited to using qualitative phrases to describe the association between a suspect and a DNA mixture. A consensus developed among the scientific community, however, that a statistic should be applied to describe more precisely any positive association between a suspect and DNA evidence.

For example, the National Research Council included in its 2009 report, "Strengthening Forensic Sciences in the United States: A Path Forward," the recommendation that a statistical weight be applied to all positive associations.[12] In 2010, the SWGDAM adopted Interpretation Guideline 4.1, which states that "the laboratory must perform statistical analysis in support of any inclusion that is determined to be relevant in the context of a case." *See* Ex. D. In addition,

[11] Available at: https://www1.nyc.gov/assets/ocme/downloads/pdf/technical-manuals/forensic-biology-technical-manuals/sample_comparisons_identifiler_and_yfiler_071919.pdf

[12] Available at https://www.ncjrs.gov/pdffiles1/nij/grants/228091.pdf

the DNA Commission of the International Society of Forensic Genetics also recommended that a likelihood ratio be applied to mixture interpretations.[13]

Consistent with this scientific consensus, and to comply with the best scientific practices, OCME developed FST to give a quantitative—*i.e.*, a statistical—way to describe the strength of the connection between an individual's DNA profile and a mixture of DNA collected from a particular sample. [14] FST is computer software that calculates "likelihood ratios," based on the extent to which the alleles in the suspect's DNA match the alleles of a DNA sample taken from evidence in the case, and how common the alleles are in the population as a whole. The likelihood ratio is then expressed as the probability of a seeing the mixture of DNA from the evidence if a suspect *did* contribute to the mixture (Scenario 1) compared with the probability of seeing the mixture if unknown persons *and not the suspect* contributed (Scenario 2). Pursuant to OCME's protocols, FST only calculates a likelihood ratio after an analyst compares the alleles of the DNA mixture to the suspect's DNA profile and determines that the suspect is included as a possible contributor. *See* Sample Comparisons Manual at 5 ("The likelihood ratio (LR) can be calculated (if appropriate) using [FST] if there is a positive association (is included) between the comparison sample(s) and the evidence sample."). Where an analyst determines that a suspect

---

[13] *See* Ex. E (Peter D. Gill *et al.*, "DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures," *Forensic Sci. Int.* 160: 90-101 (2006)) (discussion advantages of likelihood ratio and concluding that "[a] likelihood ratio approach is therefore preferred."); *see also* Ex. F (H. Haned, *et al*., "Estimating drop-out probabilities in forensic DNA samples: A simulation approach to evaluate different models," *Forensic Sci. Int.*, 525 (2011)) ("The likelihood ratio framework is the preferred approach to report the weight of DNA evidence.").

[14] *See also* Ex. G (Roberto Puch-Solis, *et al.*, "Evaluating Forensic DNA Profiles Using Peak Heights, Allowing for Multiple Donors, Allelic Dropout and Stutters," *Forensic Sci. Int.: Genetics*, 556 (2013)) ("There is now widespread agreement that the evidential weight in criminal trials is best measured via likelihood ratios comparing prosecution and defense hypothesis.")

can be excluded because the person's alleles do not match the evidence, FST is not run and no likelihood ratio is calculated. *See* Ex. B (*Jones* Tr.) at 35 ("If the analyst has determined that the person is excluded as a contributor, then no FST would be run."); *see also id.* at 143.

The likelihood ratio produced by FST is expressed as a number, and OCME offers the following corresponding qualitative interpretations:

Likelihood ratio of 1 to 10	Limited Support
Likelihood ratio of 10 to 100	Moderate Support
Likelihood ratio of 100 to 1000	Strong Support
Likelihood ratio greater than 1000	Very Strong Support

B. Development, Validation, and Implementation of FST

FST's reliability was demonstrated through a rigorous certification and validation processes and review by independent experts. As part of this process, the NYS Commission and its DNA Subcommittee approved the use of FST in criminal cases. As the Second Circuit summarized, the validation process took "a year and a half and involved extensive mock case work — processed according to OCME protocols and replicating common sources of error, such as degradation — on 439 two- and three-person, high and low-mass mixtures, far exceeding SWGDAM's recommendation of at least 50 mixtures." *Jones*, 965 F.3d at 157; *see also* Ex. B (*Jones* Tr.) at 137-55. (describing validation process, including how OCME's validation studies and data encompassed 22 volumes of two or three-inch binders). The results demonstrated that the likelihood ratios were consistent with, and more informative than, the qualitative statements that OCME provided for DNA mixture analysis prior to FST. Ex. B (*Jones* Tr.) at 146-47.

OCME further studied FST's false positive rate by comparing two- and three-person casework mixtures with DNA from over 1,200 individuals who were known non-contributors.

Jones, 965 F.3d at 157. The tests demonstrated that FST had a very low false positive rate. Of the more than a half million tests performed, only 163 were false positives. *Id.* FST's overall false positive rate was thus .03%. *Id.* And the false positives decreased significantly as the likelihood ratio increased: where FST indicated limited support (a likelihood ratio of 1 to 10), the false positive rate was .01%. Ex. B (*Jones* Tr.) at 151. Where FST indicated very strong support (a likelihood ratio over 1,000), the false positive rate was .0009%. *Jones*, 965 F.3d at 157. And where the FST was over 10,000, as in Cortorreal's case, there was just one documented instance where a match was erroneously indicated. Ex. B (*Jones* Tr.) at 151.

A summary of the validation studies was published in a peer-reviewed journal and FST has been the subject of numerous industry presentations and workshops. *Id.* at 81.

C. The 97 Allele Cap Modification

Following the NYS Commission's approval of FST in April 2011, OCME began to use FST. Shortly thereafter, FST generated a negative likelihood ratio, which did not make mathematical sense. *See Jones* Tr. 396-97. OCME took FST offline, investigated, and discovered that shortly after FST's approval, programmers had updated some functions and a small, unrelated change was inadvertently made to the source code that affected the way numbers were sorted in certain instances. Silverman Ex. C (Adams Decl. Appendix 4) (Oct. 18, 2017 letter from OCME General Counsel); *see also*, Ex. B (*Jones* Tr.) at 398-99.

While investigating this issue, OCME determined that FST could also potentially calculate a negative likelihood ratio if the allele frequencies at a locus added up to over 1 — meaning that more than 100 percent of the population had the alleles present at the locus. *See* Ex. B (*Jones* Tr.) at 400. OCME discovered that FST could potentially calculate this mathematical impossibility because of two conservative adjustments that were incorporated into

FST. As Dr. Mitchell testified in *Jones*, these two adjustments "are standard measures that . . . many if not all labs use with random match probability." *Id.* at 172. First, if an allele is extremely rare, or not observed in the frequency database that the lab uses, "there is a standard protocol that is to assume that it was seen five times in the sample." *Id.* This change, which is recommended by the National Research Council,[15] typically benefits *the defendant*, not the Government, as it ensures that if the suspect has a very rare allele that is present in the mixture, it is not given too much weight: "[i]t's a way of down-weighting super rare alleles." Ex. B (*Jones* Tr.) at 172. Second, if a population is not freely mixing, there is a greater frequency of loci with homozygotes, meaning locations where a person receives the same allele from both parents. Accordingly, "[OCME] and other forensic labs make slight adjustment[s] to the expected frequency of homozygous genotypes." *Id.*

Taken together, the two changes meant that if a locus had alleles that added up to almost 1, the adjustments could increase the frequency above 1 and trigger a negative likelihood ratio. *Id.* at 173. To address this potential issue, OCME revised FST so that any locus where the allele frequency added up to .97 or higher was treated as "1," (referred to herein as the "97 Allele Cap") and the locus was therefore considered uninformative. *Id.* at 174. In other words, while the defendant may have the very same alleles at that locus (and therefore would seem a more likely contributor to the comparison sample), because the alleles are so prevalent in the population generally, the source code treats this scenario as making it neither more nor less likely that the defendant contributed to that locus. After implementing the 97 Allele Cap, OCME conducted a performance check and found that the cap did not significantly impact the likelihood ratio calculations. *Id.* at 177-181 (describing the results of the performance check).

[15] *See* National Research Council, The Evaluation of Forensic DNA Evidence, (1996) at 29-30, 122, available at https://www.ncbi.nlm.nih.gov/books/NBK232610/.

OCME stopped using LCN and FST for new casework in January 2017. The decision was the result of a change to the FBI's national database of DNA profiles ("CODIS"). Ex. B (*Jones* Tr.) at 68-71. While CODIS previously required data from 13 loci in order to load a profile in the database, it increased the requirement to 20 loci as of January 2017. *Id.* at 68. Because the amplification kit with which LCN and FST had been validated amplified data at 15 loci, OCME would have had to upgrade its amplification kit and then revalidate both LCN and FST for use with that particular amplification kit. *Id.* at 70. Rather than engage in that costly and time-consuming process, OCME switched to a commercially available likelihood ratio program. *Id.* at 70-71. OCME continues to use FST on samples that were amplified prior to January 2017.

V. The Second Circuit Upholds the Reliability and Admissibility of LCN and FST

As described below, many of the arguments defendant raises in this case were raised and rejected in *United States v. Morgan* and *United States v. Jones*. In each of those cases, the Court denied the defendant's *Daubert* motion and the Second Circuit affirmed. Each of these cases is discussed further below.

A. *United States v. Morgan* and the Reliability of LCN

In *Morgan*, the defendant was charged with being a felon in possession of a firearm and moved to exclude DNA evidence from the gun at issue, challenging OCME's use of LCN testing. *See Morgan*, 53 F. Supp. 3d at 733. Specifically, OCME used LCN to analyze 14 picograms of DNA, concluded that there were at least two contributors to the sample, identified a major contributor, and concluded that the defendant could be the source of the DNA. *Id.* at 736. Defendant sought to exclude the evidence based on a range of challenges to OCME's LCN testing. For example, defendant claimed that OCME's validation studies did not support the

LCN testing protocols and that LCN could not reliably be used to test a degraded, mixed sample, with just 14 picograms of DNA. *Id.* at 741. Defendant further claimed that using LCN to test just 14 picograms of DNA created too many stochastic effects to produce a reliable result. *Id.* at 743. Defendant also alleged that OCME had incorrectly concluded that there were two contributors to the sample, when in fact, pursuant to OCME's own protocols, there were at least three contributors. *Id.* at 745-46. In particular, defendant cited the fact that one locus had five repeating alleles and another locus had seven repeating alleles. *Id.*

After multiple rounds of briefing and a three-day *Daubert* hearing, where each of these issues were addressed in detail, Judge Marrero denied the defendant's motion, finding that "the overwhelming weight of the evidence . . . demonstrates that OCME's LCN testing methodology is firmly rooted in science." *Id.* at 744; *see also id*. at 733 (holding that "the methods of LCN DNA testing that [OCME] employed are sufficiently reliable to satisfy the *Daubert* standard"). In so holding, Judge Marrero noted "[e]ach of the three characteristics of the crime scene sample that [defendant] has presented as problematic — the small quantity, the mixed DNA, and the degradation — was tested in OCME's validation studies . . . [and] taken together, they formed the basis for robust and reliable interpretation protocols. . . ."). With respect to the number of contributors, the Court found that defendant's argument based on the number of alleles was "overly simplistic" in failing to recognize "stochastic effects such as allelic drop-in," and that the "DNA analyst in this case was well within the proper scope of her discretion to determine that the sample included two or more individuals." *Id.* at 746. The defendant's arguments to the contrary represented "another example of a disagreement based on an alternative interpretation of the same data," and was thus an appropriate subject for cross-examination, not a basis for exclusion. *Id.*

The Second Circuit noted that while LCN was supported by less evidence of reliability than traditional DNA analysis, the district court did not abuse its discretion in holding that the evidence was admissible. *United States v. Morgan*, 675 Fed. App'x 53, 55-56 (2d. Cir. 2017).

B. *United States v. Jones*

1. Judge Broderick's Comprehensive Daubert Hearing

In *Jones*, the defendant was charged with one count each of Hobbs Act conspiracy, Hobbs Act robbery, and possession of a firearm, which was discharged, in furtherance of the Hobbs Act crimes, in connection with a robbery where a victim was shot in the leg. *Jones*, 965 F.3d at 153. The Government sought to introduce DNA evidence from a glove found where one of the robbers fled. *Id.* at 154. OCME analyzed the DNA from the glove swab and concluded that there were at least three contributors, that Jones could not be excluded, and using FST, that it was 1,340 times more likely that Jones and two unknown, unrelated individuals contributed to the mixture as compared to three unknown, unrelated individuals having contributed to the mixture. *Id.* at 156.[16] Accordingly, OCME concluded that there was "very strong" support for the conclusion that Jones contributed to the mixture. *Id.*

In November 2015, defendant moved to exclude the DNA evidence from the glove, raising a host of challenges under *Daubert*, including that FST was unreliable. *Jones* Doc. 16. The parties fully briefed the motion and submitted additional rounds of briefing addressing further issues pertaining to FST. *See Jones* Doc. 19, 21, 23, 24, 29, 30, 292, 298, 299, 302, 387. In November 2017, the Court held a comprehensive five-day *Daubert* hearing, involving live testimony from four individuals: the Government called Dr. Craig O'Connor, then Assistant Director at OCME's Department of Forensic Biology, (*Jones* Doc. 427, Tr. 2-84), and Dr. Adelle

[16] As described below, in Cortorreal's case, the likelihood ratio is 11,480, more than eight times greater than *Jones*, and uses the same qualitative conclusion of "very strong" support.

Mitchell, a former employee of OCME who helped develop FST (*Jones* Doc. 427, Tr. 84-186); Jones called Dr. Eli Shapiro, a former OCME employee, (*Jones* Doc. 433, Tr. 487-588) and Nathaniel Adams, a graduate student at Wright State University, with a bachelor's degree in computer science, and the same declarant in this Court's present motion. (*Jones* Doc. 435, Tr. 684-770). Jones further submitted the prior testimony of Dr. Ranajit Chakraborty, who was a member of the DNA Subcommittee that approved FST.

Through the extensive briefing, *Daubert* hearing, and oral argument, the parties addressed a wide array of challenges to OCME's DNA testing generally, and the use of FST specifically. For example, Jones claimed that OCME was wrong in concluding that there were at least three contributors to the DNA swab, because there were at least four contributors. Ex. B (*Jones* Tr.) at 522, 528, 897-98. Jones further claimed that FST was unreliable because it relied on an estimate of the number of contributors, which, if wrong, rendered the likelihood ratio irrelevant. *See, e.g.*, *Jones* Doc. 16, at 9, 17-19; Ex. B (*Jones* Tr.) at 208-13, 531-37, 897-98. In connection with these arguments, the Court heard detailed testimony about how OCME's analysts determine the number of contributors, how OCME's related protocols were validated and reviewed by OCME's accrediting bodies, and defendant's criticisms of OCME's processes and protocols. *See, e.g.*, Ex. B (*Jones* Tr.) at 25-29. 62-64, 204-19, 270, 428-31, 532-41, 641-42, 647-51.

Jones further claimed that the 97 Allele Cap made FST unreliable because it impacted the likelihood ratio and was a significant change that should have required revalidating FST. *Jones* Doc. 299, at 4-5. Jones noted that in his case, the 97 Allele Cap resulted in three loci being "dropped," which led to less accurate results. Ex. B (*Jones* Tr.) at 900. The Court accordingly heard testimony and received briefing on why the 97 Allele Cap was created, how it might

impact the likelihood ratio, and the performance checks OCME did to ensure it did not undermine the reliability of the likelihood ratios, including defendant's criticisms of those checks. *See, e.g.*, *Jones* Docs. 299, 302; Ex. B (*Jones* Tr.) at 172-85, 256-67, 396-415, 574-87, 741-56, 892-97.

Jones also argued that FST failed to comply with software engineering standards, and Adams submitted a declaration describing such concerns and further testified at length on the issue. *See Jones* Doc. 299 and 299-2; Ex. B (*Jones* Tr.) at 722-36; *see also id.* at 867-69 (Jones discussing the issue at oral argument). Of note, Judge Broderick qualified Adams as an expert in computer science, but would not qualify him as an expert in bioinformatics. *Id.* at 717-18.[17]

Finally, Jones argued more generally that because OCME was developed in-house and not used by other labs, it had not gained sufficient acceptance within the scientific community and had not been subject to sufficient peer review. *Jones* Doc. 16, at 16-17.

Following the hearing and Judge Broderick's consideration of what he referred to as an "extensive record" the Court held that "expert testimony on the FST in this case rests on a reliable foundation and is relevant to the task at hand." *Jones*, 2018 WL 2684101, at *12. In reaching this decision, the Court noted that "the use of FST evidence in courts is by no means new or novel — state courts have repeatedly admitted FST evidence as reliable, even under the less permissive standard annunciated in *Frye v. United States*, 293 F. 1013 (D.C. Cir. 1923)." *Id.* at *8. The Court also found that "not only has FST evidence been routinely introduced at criminal trials by the prosecution (*i.e.*, where the FST's LR tends to implicate a defendant), but

[17] Adams had no degree in forensics, no graduate degree in statistics, had never worked in a forensic lab, never done DNA testing on a piece of evidence, had no peer-reviewed publications, and a prior court had refused to qualify him as an expert in DNA data analysis. *Id.* at 711-14; *see also id.* at 483-84 (Judge Broderick: "[j]ust on the basis of his background, I have serious questions about whether or not the presentation, in terms of being before a jury, whether or not I would allow him to do that. Computer science, that's a different issue.").

also by the defense (*i.e.*, where the FST's LR tends to exculpate a defendant)." *Id.* at *9.

Judge Broderick thereafter applied the *Daubert* factors, noting that the only two factors in meaningful dispute were the known or potential error rate of FST, and the general acceptance of FST in the scientific community. *Id.* The Court explained that although FST did not have a known or potential error rate — because the number of contributors could not be determined with certainty — OCME's validation studies showed "FST's false positive rate to be very low." *Id.* OCME's validation study further "showed that as the LR increased, the false positive rate decreased dramatically," such that for a likelihood ratio of between 1,000 and 10,000, which the Government was seeking to introduce in *Jones*, the false positive rate was just 0.009%. *Id.*

In addressing FST's general acceptance in the scientific community, the Court reiterated that "nearly every court to have considered the FST has found it to be a reliable tool that is generally accepted by the scientific community," and "FST has been approved for use in casework by members of the relevant scientific community and subjected to peer review." *Id.* at *10. The Court also rejected Jones's argument that FST was unreliable because it relied on too many assumptions or estimations, reasoning that defendant "is unable to point to any study, article, or presentation that confirms that FST is not a proper tool." *Id.* The Court found that "[e]ach of the assumptions incorporated into FST . . . has been the subject of exhaustive testing, validation, peer review, accreditation, auditing, and other review processes described above." *Id.* The Court explained that "[i]n any event, cross-examination at trial is the more appropriate avenue for Defendant to mount his challenges to the underlying components of the FST.'" *Id.*

In summary, the Court reiterated that "FST has been rigorously tested and subjected to peer review. OCME performed validation studies of its methods, published those studies in a peer-reviewed journal, and the DNA Subcommittee approved the FST testing for use in criminal

casework." *Id.* at *12. The Court further explained that "[t]o the extent the Defendant disagrees on how the FST was applied in this particular case, he can address those concerns at trial by putting on expert testimony and cross-examining witnesses, allowing the jury to make any such determination as to the application of the FST." *Id.*

2. The Second Circuit Affirms Judge Broderick's Decision

In July 2020, the Second Circuit affirmed Judge Broderick's ruling, holding that "[w]e are unpersuaded that there was any abuse of discretion in the district court's conclusion that FST evidence was sufficiently reliable to be admitted in evidence and [] Jones's contrary contentions go to the weight of that evidence, not to its admissibility." *United States v. Jones*, 965 F.3d 149, 161 (2d Cir. 2020). The Court described how Judge Broderick's five-day *Daubert* hearing "exhaustively dissected FST's development, methodology, and implementation." *Id.* at 162. The Court further addressed the disputed *Daubert* factors. With respect to error rate, the Court noted "FST's overall false-positive rate is 0.03 percent, a mere three-hundredths of one percent; and that for 'very strong support' likelihood ratios (*i.e.*, those more than 1,000) — including that for the Glove DNA here . . . the false-positive rate is a mere 0.0009 percent." *Id.* With respect to FST's general acceptance, the Court held that FST's admission in "scores of New York cases,"[18] and "'the fact that the FST has been approved for use in casework by members of the relevant scientific community and subject to peer review,'" supported its admission. *Id.*

VI. The DNA Evidence in Cortorreal's Case

After running LCN on the Cellphone Battery Swab and the Duct Tape Swab, and

[18] Defendant claims that the caselaw regarding the admissibility of FST differs within New York's own courts, but defendant cites only one case excluding the evidence and one case holding that the lower court should have held a *Frye* hearing before admitting FST. However, as stated in *Jones*, the vast majority of New York cases have admitted FST evidence.

analyzing the results, OCME summarized its findings in an April 4, 2007 report. *See* Silverman Ex. M. For the cellphone battery, OCME was able to discern a partial profile, with 11 loci, which it labeled "Male donor B," and concluded that the DNA profile would be expected to be found in approximately 1 in 400 million people. *Id*. at 3.[19]

For the Duct Tape Swab, OCME concluded that the results showed "a mixture of DNA from at least three people." *Id.* OCME was unable to discern a major profile, but compared the alleles to the Male donor B profile from the Cellphone Battery Swab, and concluded that "Male donor B could have contributed to this mixture." *Id.*

On February 5, 2020, the Honorable Sarah Netburn, United States Magistrate Judge for the Southern District of New York, signed a search warrant authorizing law enforcement to obtain oral swab DNA samples from Cortorreal, which law enforcement collected and sent to OCME for testing and analysis. As explained in the casefile, the assigned case analyst and technical reviewer, who were different from the analyst and reviewers who examined the evidence in 2007, "completed a review of all case records pertaining to this Forensic Biology case number . . . . the case Analyst(s) and Technical Reviewer(s) personally examined each peak at each locus to make their own determination as to whether that peak represents the DNA present." Silverman Ex. A at Cortorreal_000032. After a complete review, "the case Analyst(s) and Technical Reviewer(s) made independent interpretations, conclusions and comparisons of all analyses and results." *Id.* On April 16, 2020 OCME issued a report summarizing its findings.

First, OCME concluded that Cotorreal's DNA profile matched the profile of "Male donor

[19] On April 10, 2015, OCME amended the April 2007 report, identifying 13 loci from the Cellphone Battery Swab (as opposed to 11 loci) and concluding that this DNA profile would be expected to be found in approximately 1 in 176 billion people. OCME's conclusions regarding the Duct Tape Swab did not change in the amended report.

B" from the Cellphone Battery Swab, and that the DNA profile would be expected to be found in approximately 1 in 50.4 billion people. *Id.* at Cortorreal_000031. Second, OCME compared Cortorreal's DNA profile to the Duct Tape Swab, saw that Cortorreal's alleles were present in the composite at every single one of the 15 loci, and concluded that Cortorreal was included as a possible contributor.[20] *Id.* OCME further concluded, consistent with the April 2007 report, that the Duct Tape Swab was a mixture with at least three contributors. *Id.* OCME thus used FST to calculate a likelihood ratio, finding that the DNA mixture from the Duct Tape Swab "is approximately 11,400 times more probable if the sample originated from Edwin Cortorreal and two unknown, unrelated persons, than if it originated from three unknown, unrelated persons." *Id.* Using OCME's verbal scale, OCME concluded that there was "very strong support" for the conclusion. *Id.*

ARGUMENT

I. Applicable Law

Under Federal Rule of Evidence 702, the Court may admit "[a] witness who is qualified as an expert . . . if: (a) the expert's scientific . . . knowledge will help the trier of fact to understand the evidence or to determine a fact in issue; (b) the testimony is based on sufficient facts or data; (c) the testimony is the product of reliable principles and methods; and (d) the expert has reliably applied the principles and methods to the facts of the case." Fed. R. Evid. 702; *see also Daubert* v. *Merrell Dow*, 509 U.S. 579, 592-93 (1993) (explaining that the district court must assess "whether the reasoning or methodology underlying the [expert's] testimony is

[20] As the April 16, 2020 appendix explained, an individual "is included as a possible contributor" when for the loci where comparisons can be made "all or almost all of the DNA alleles seen in an individual's DNA profile were also seen in the mixture." Silverman Ex. A at Cortorreal_000033.

scientifically valid and . . . whether that reasoning or methodology properly can be applied to the facts in issue").

The proponent of expert testimony has the burden of establishing by a preponderance of the evidence that the admissibility requirements of Rule 702 are satisfied. *See Daubert*, 509 U.S. at 593 n.10. The district court plays a gatekeeping role, which requires the court to "'make certain that an expert . . . employs in the courtroom the same level of intellectual rigor that characterizes the practice of an expert in the relevant field.'" *Amorgianas* v. *Nat'l R.R. Passenger*, 303 F.3d 256, 265-66 (2d Cir. 2002) (quoting *Kumho Tire Co., Ltd.* v. *Carmichael*, 526 U.S. 137, 150 (1999)).

In *Daubert*, the Supreme Court set out a list of non-exclusive factors that the trial court may consider in determining whether an expert's reasoning or methodology is reliable: (1) whether the theory or technique used by the expert can be, or has been, tested; (2) whether the theory or technique has been subjected to peer review or publication; (3) the known or potential rate of error of the method used; (4) whether there are standards controlling the technique's operation; and (5) whether the theory or method has been generally accepted within the relevant scientific community. *Daubert*, 509 U.S. at 593-94.

Significantly, the *Daubert* test replaced the test set forth in *Frye* v. *United States*, 293 F. 1013 (D.C. Cir. 1923), which required that expert testimony be generally accepted among the scientific community, and which is still used by state courts in New York. The *Daubert* test "embodies a more liberal standard of admissibility for expert opinions" than the *Frye* standard.[21]

[21] Under *Frye*, the proponent of a scientific technique had to establish the general acceptance of the reliability of the technique within the relevant scientific community. Even under *Frye*, however, the technique at issue did not have to be unanimously accepted by the scientific community. *See, e.g.*, *People v. Middleton*, 54 N.Y.2d 42, 49 (1981) ("But the test is not whether a particular procedure is unanimously indorsed by the scientific community, but whether

United States v. *Williams*, 506 F.3d 151, 161-62 (2d Cir. 2007) ("*Daubert* did make plain that Rule 702 embodies a more liberal standard of admissibility for expert opinions than did *Frye* v. *United States*, 293 F. 1013, 1014 (D.C. Cir. 1923)") (citations omitted); *see also Daubert*, 509 U.S. at 588 (the Federal Rules adopted a "liberal thrust" and a "general approach of relaxing the traditional barriers to 'opinion' testimony") (quoting *Beech Aircraft Corp.* v. *Rainey*, 488 U.S. 153, 169 (1988)). Moreover, the Supreme Court cautioned district courts that in carrying out their gatekeeper function, "vigorous cross-examination, presentation of contrary evidence, and careful instruction on the burden of proof are the traditional and appropriate means of attacking shaky but admissible evidence." *Daubert*, 509 U.S. at 596.

The Second Circuit has consistently applied this broad standard in determining the admissibility of expert opinion testimony under Rule 702 and *Daubert*. *See, e.g.*, *Boucher v. United States Suzuki Motor Corp.*, 73 F.3d 18, 21 (2d Cir. 1996) ("Although expert testimony should be excluded if it is speculative or conjectural, or if it is based on assumptions that are so unrealistic and contradictory as to suggest bad faith or to be in essence an apples and oranges comparison, other contentions that the assumptions are unfounded go to the weight, not the admissibility, of the testimony.") (citations and internal quotation marks omitted); *see also Travelers Property & Cas. Corp.* v. *General Elec. Co.*, 150 F. Supp. 2d 360, 363 (D. Conn. 2001) (noting that a "review of the case law after *Daubert* shows that the rejection of expert testimony is the exception rather than the rule." (quoting Advisory Committee's Notes on 2000

---

it is generally acceptable as reliable."). Seventy years after the *Frye* decision, the Supreme Court in *Daubert* set aside *Frye* as a matter of federal evidentiary law. All federal courts and those of many states have adopted the *Daubert* standard. Because the rule of *Daubert* constituted an interpretation of the Federal Rules of Evidence, it was not mandated as a matter of constitutional law. Thus, the states were free to accept *Daubert* or continue to adhere to *Frye* in deciding when expert testimony should be admitted at trial. New York has continued to adhere to the *Frye* standard.

Amendments to Fed. R. Evid. 702)). Indeed, the Second Circuit has explained that, at bottom, the *Daubert* analysis is intended to give the district court the discretion "needed to ensure the courtroom door remains closed to junk science while admitting reliable expert testimony that will assist the trier of fact." *Amorgianos*, 303 F.3d at 267.

In considering a *Daubert* challenge, the Second Circuit has also emphasized that the proper focus of a court's review is on the process of the science, not the results. "[T]he district court must focus on the principles and methodology employed by the expert, without regard to the conclusions the expert has reached or the district court's belief as to the correctness of those conclusions." *Amorgianos*, 303 F.3d at 266 (*citing Daubert*, 509 U.S. at 595). In evaluating the challenged process, courts may nevertheless consider the application of the science in the instant case, in order to prevent "too great an analytical gap between the data and the opinion proffered." *Id.* (citing *Gen. Elec. Co.* v. *Joiner*, 522 U.S. 136, 146 (1997)).

As the Second Circuit has recognized, however, this is a relatively limited inquiry. It is not an inquiry into whether the process was applied perfectly, or whether anyone could disagree with the application of the process in this case. The Second Circuit has explained that "[a] minor flaw in an expert's reasoning or a slight modification of an otherwise reliable method will not render an expert's opinion per se inadmissible." *Id.* at 267. Rather, the "judge should *only* exclude the evidence if the flaw is large enough that the expert lacks 'good grounds' for his or her conclusions." *Id.* at 267 (internal citations and quotation marks omitted).

Finally, while district courts must exercise the gatekeeping function regarding expert testimony, a separate hearing is often not required. *Williams*, 506 F.3d at 161 (citing *Kumho Tire*, 526 U.S. at 152 (district courts possess "latitude in deciding how to test an expert's reliability, and to decide whether or when special briefing or other proceedings are needed to

investigate reliability") and *United States* v. *Alatorre*, 222 F.3d 1098, 1102 (9th Cir. 2000) ("Nowhere . . . does the Supreme Court mandate the form that the inquiry into . . . reliability must take . . . ."). "This is particularly true if, at the time the expert testimony is presented to the jury, a sufficient basis for allowing the testimony is on the record." *Williams*, 506 F.3d at 161 (citing 4 Weinstein's Federal Evidence § 702.02[2] (Joseph M. McLaughlin ed., 2d ed. 2006)).

II. Discussion

As described below, almost all of defendant's arguments were raised and rejected in *Morgan* and *Johnson* and should similarly be rejected in this case as they are unpersuasive and, at best, go to the weight of the evidence and not its admissibility. The few additional arguments do not impugn the validity and reliability of OCME's processes and do not support reaching a different conclusion here. Moreover, given the voluminous record developed in both *Morgan* and *Johnson*, a further *Daubert* hearing is unnecessary. *See Jakobetz*, 955 F.2d at 799 ("[W]e do not think that such extensive hearings and findings should be conducted in every case"). As the Second Circuit has held, where a similar evidentiary issue was addressed in a prior case, "a court could properly take judicial notice of the general acceptability of the general theory and use of the specific techniques." *Id.*

Ultimately, none of defendant's arguments, alone or taken together, support that the DNA evidence from the Duct Tape Swab was the result of junk science or so speculative or conjectural as to suggest bad faith, and thus do not meet the requirements for exclusion under *Daubert*.

A. OCME Properly Concluded that There were At Least Three Contributors to the Duct Tape Swab

One of defendant's main arguments in seeking to exclude the DNA evidence from the Duct Tape Swab is that OCME incorrectly concluded that there were at least three contributors.

According to the defendant, "[i]t is clear that the Duct Tape Sample contains at least four, maybe even five or more contributors." Br. at 18.[22] As described below, OCME's finding that there were at least three contributors was a reasonable conclusion independently reached by four different analysts and a proper application of OCME's protocols. As both *Morgan* and *Jones* have held, defendant's arguments to the contrary go to the weight, not admissibility of the evidence.

OCME analysts determine the number of contributors based on a review of the entire set of DNA results, including the composite profile, which is comprised of all alleles present in at least two of the three amplifications. STR Results Interpretation Protocol at 11, 41. Specifically, analysts look at the number of alleles at each locus, taking into consideration that, in general, each person has two alleles at any locus, but stochastic effects can impact the number of observed alleles. OCME developed protocols based on empirical studies to help guide analysts in determining the number of contributors. These protocols take into account the risk of stochastic effects, are reviewed by OCME's accrediting bodies, consistent with SWGDAM guidelines, and generally accepted in the scientific community. *See* Ex. B (*Jones* Tr.) at 28-30, 205, 270. Pursuant to OCME's protocols for LCN testing, three-person mixtures occur where "five alleles are present in at least two loci in the composite." STR Results Interpretation Protocol at 42. Four-person mixtures occur where the composite has seven or more alleles in at least two or more loci. *Id*.

Below is a copy of the allele calls from Cortorreal's DNA swab and the three

[22] Defendant's argument relies on the declaration of Dr. Dan Krane. Of note, in *United States v. Gissantaner*, the Sixth Circuit overruled a district court opinion that excluded DNA evidence based on the opinion of Dr. Krane, who was appointed as an independent expert. As the Sixth Circuit noted, "Dr. Krane, was not as independent as the court suggested. He was the president of the firm that employed [defendant's] expert, and he had previously worked on the case for [defendant]." 990 F.3d 457, 469 (6th 2021).

amplifications of the Duct Tape Swab. The top row lists the name of the locus analyzed, the columns below contain the allele calls at each locus, with the second row being the allele calls for Edwin Cortorreal, and the three white horizontal rows contain the allele calls for each of the three amplifications of the Duct Tape Swab (referred to as tape_a, tape_b, and tape_c).

determination, therefore these additional peaks are not reported.

FBS20-00663

Sample description	D8S1179 1	D21S11 1	D7S820 1	CSF1PO 1	D3S1358 1	TH01 1	D13S317 1	D16S539 1	D2S1338 1	D19S433 1	vWA 1	TPOX 1	D18S51 1	AMEL 1	D5S818 1	FGA 1	DNA AMP'D
Edwin Cortorreal	13,14	29,30.2	10	10,11	14,16	7,8	11,12	9,13	19,23	14	14,16	8,9	15,16	X,Y	12,13	22,26	
swab 1B from the "roll" of "gray duct tape"																	
FB06-1922 swab 1B from 'duct tape'_a HS1010807_36N HS1010907_45L	13 14 15 16	29 30 30.2 32.2	9 10 11	10 11 12 13	14 15 16 17	7 8 9 9.3	8 10 11 12 13	9 10 11 12 13	17 19 23 24	12 13 14 15	14 15 16 18 19	6 8 9 10 11	12 15 16	X Y	10 11 12 13	22 23 24 26	
FB06-1922 swab 1B from 'duct tape'_b HS1010807_36N HS1010907_45L	13 14 15 16	29 30 30.2 32.2	9 10 11 12	9 10	14 15 16 17	6 7 8 9	8 11 12 13	9 11 12	18 19 23 24	12 13 14 15	13 14 15 16 18 19	6 8 9 10 12	12 15 16 19 20	X Y	10 11 12 13	19 22 23 24 26	
FB06-1922 swab 1B from 'duct tape'_c HS1010807_36N HS1010907_45L	12 13 14 15 16	29 30 30.2 32.2	9 10	9 10 11	14 15 16 17	6 7 8 9 9.3	8 11 12 13 14	9 11 12 13	19 21 23	12 13 14 15	13 14 15 16 17 19	6 8 9 10 11 12	12 14 15 16	X Y	10 11 12 13	22 23 24 26	
Composite[A] profile	13, 14, 15, 16	29, 30, 30.2, 32.2	9, 10, 11	9, 10, 11	14, 15, 16, 17	6, 7, 8, 9, 9.3	8, 11, 12, 13	9, 11, 12, 13	19, 23, 24	12, 13, 14, 15	13, 14, 15, 16, 18, 19	6, 8, 9, 10, 11, 12	12, 15, 16	X Y	10, 11, 12, 13	22, 23, 24, 26	100
Mixture for comparison																	

Silverman Ex. A-2 at Cortorreal_000058.

As reflected in the above, the composite profile for the Duct Tape Swab did not contain any locus with seven alleles.[23] In fact, no locus in any single amplification (*i.e.*, tape_a, tape_b or tape_c) had seven alleles. And the composite profile had only two loci with six alleles and one locus with five alleles; all other loci had three or four alleles. Accordingly, OCME analysts properly determined that the Duct Tape sample had at least three contributors. An OCME analyst first reached this conclusion when the evidence was analyzed in 2007, years before FST was created. *See* Silverman Ex. M. OCME's Assistant Director thereafter reviewed the casefile and report and agreed with that conclusion. In 2020, a different analyst reviewed the entire casefile and made a new and independent determination that the sample was a three-person mixture, and that conclusion was again reviewed by a different Assistant Director and Technical Leader, Dr. Craig O'Connor, who further reviewed the casefile and agreed with the

[23] As described above, in *Morgan*, the DNA sample had seven *repeating* alleles, and yet OCME concluded that there were *two* contributors, and Judge Marrero nevertheless found that OCME's process was reasonable and the evidence was admissible.

determination. *See* Silverman Ex. A at Cortorreal_000031 and Ex. A-2 at Cortorreal_000062.

Defendant claims that OCME's analysts were all wrong and that the Duct Tape Swab has at least four contributors because one locus has seven alleles. As defendant explains, because each person receives one allele from each parent, a seventh allele necessarily demonstrates the presence of four contributors. Br. at 18. In arguing that one locus had seven alleles, defendant appears to be counting the total number of alleles identified across all three amplifications of the locus "vWA 1," highlighted in the red box. But even at that locus, each amplification only identified six alleles. And as defendant recognizes in criticizing the increased risk of stochastic effects from LCN testing, the presence of a seventh allele, particularly at one locus, could be explained by the stochastic effects of allele drop-in or elevated stutter. Br. at 18. It is for that very reason that OCME's protocols look for *multiple* loci with seven or more *repeating* alleles before determining that the sample has at least four contributors.

Defendant next claims that the Duct Tape Swab has at least four contributors because it has a total of 76 alleles and a 2011 OCME research paper examined a set of two-, three-, and four-person mixtures and found that the maximum number of alleles for the observed three person mixtures was 66 and four person mixtures was 75. Br. at 18-19. In addition, defendant claims that the Duct Tape Swab has five of the eight factors that the study identified as characteristics of mixtures with more than three contributors. *Id.* Contrary to defendant's claims, the 2011 OCME paper was not a validation study, but a research paper intended to be used as a reference point. In describing the total number of alleles and common characteristics seen in the mixtures with four contributors, the paper was not purporting to establish strict thresholds for future analysis, and OCME has not used it in that manner. *See* Silverman Ex. F at 325 ("The success rates stated here are data driven estimates and may not be representative of

all forensic samples. Although a variety of template amounts and mixture ratios were included in this sample set, forensic samples may exhibit qualities not observed in these mixtures."). Moreover, only three of the eight characteristics associated with four-person mixtures are present in the Duct Tape Swab: 5 or more loci with 6 different alleles (Duct Tape Swab had 5 loci); 8 or more loci with five different alleles (Duct Tape Swab had 8 loci); and more than 13 loci with more than 4 different alleles (Duct Tape Swab had 15 loci).[24]

Ultimately, as both *Morgan* and *Johnson* recognized, arguments about the number of contributors go to the weight and not admissibility of the evidence, and thus do not support excluding the evidence under *Daubert*. For example, in *Morgan*, according to defendant's arguments, the sample had even more indicia of four or more contributors, because the sample had a locus with seven repeating alleles, but OCME concluded that the sample was a two-person mixture. 53 F. Supp. 3d at 745. The Court summarily rejected defendant's argument that the number of alleles was necessarily indicative of more contributors, finding that it was "overly simplistic, in that it fails to acknowledge that extra alleles can appear because of stochastic effects such as allelic drop-in." *Id.* at 746. The Court noted that the defendant was "quick to point to the presence of stochastic effects in LCN testing when arguing that such stochastic effects make LCN testing unreliable, but conveniently disregards [them] . . . when claiming that the presence of more than five alleles at a locus must indicate the contribution of DNA from at least three individuals." *Id.* The Court further characterized the argument as "another example of disagreement based on an alternative interpretation of the same data," which "falls within the provenance of the jury." *Id.* Here, defendant makes the same argument, which should be rejected for the same reasons.

[24] Defendant is incorrect in claiming, without explanation, that the Duct Tape Sample had 6 or more loci with 5 or more repeating alleles, or 13 loci with 4 or more repeating alleles. Br. at 19.

Defendant argues that because OCME misclassified the Duct Tape Sample as a three-person mixture, the FST likelihood ratio is unreliable and irrelevant and should not have been run since FST is not validated for four-person mixtures. Br. 20-21. A similar argument was raised and rejected in *Jones*, where defendant also claimed that the mixture had at least four contributors. Ex. B (*Jones* Tr.) at 522, 528, 897-98. As the Second Circuit noted, one of defendant's main challenges to FST was that "'so much of what [FST does] is based on estimation,' including . . . the number of contributors to a sample." *Jones*, 965 F.3d at 161. In rejecting this argument, the Second Circuit held that such arguments "go to the weight of that evidence, not to its admissibility." *Id. see also id.* at 157 (recognizing that "OCME also limited FST analysis to two- and three-person samples, because the greater the number of contributors, the higher the drop-out rate"). Moreover, it is well-established in the forensic community that likelihood ratios are valid and useful even though the true number of contributors to a sample is never known. *See* Ex. H (John Buckleton *et. al*, "Towards Understanding the Effect of Uncertainty in the Number of Contributors to DNA Stains," *Forensic Sci. Int.* (2007)) at 21; Ex. B (*Jones* Tr.) at 428-30. As described above, OCME analysts reasonably concluded that the Duct Tape Sample is a three-person mixture, and thus reasonably calculated a likelihood ratio based on three contributors. Defendant's arguments to the contrary are, at best, a subject for cross examination and not a basis for excluding the evidence.

B. OCME Properly Determined that there is Very Strong Support that Cortorreal is a Contributor

Defendant claims that OCME's conclusion that there is "very strong support" that Cortorreal contributed to the DNA on the Duct Tape Swab, is subjective, misleading, and prejudicial. Br. at 21. In support, defendant claims that OCME's verbal scale is different from that used by other laboratories. Br. at 22. However, OCME's verbal scale was adapted from

verbal scales published in two industry textbooks. *See* Ex. I (John Butler, Forensic DNA Typing, (2005); Ex. J (Evett and Weir, Interpreting DNA Evidence, (1998). The mere fact that another lab may use a different scale does not render OCME's scale arbitrary or misleading.

Once again, defendants raised a similar argument in *Jones*, challenging OCME's use of the same "very strong support" language. *See* Ex. B (*Jones* Tr.) at 855; *Jones*, 955 F.3d at 161 ("[Defendant] also complains of the decision to use a qualitative, verbal scale for reporting results"). However, Judge Broderick and the Second Circuit ultimately rejected Jones's *Daubert* motion and allowed the Government to use the "very strong support" language at trial along with the likelihood ratio of 1,340. Defendant fails to identify any reason for a contrary result here, where the likelihood ratio is 11,400 — *eight* times higher than *Jones*.

C. OCME Properly Utilized the Scientifically Valid LCN Analysis

Defendant claims, based on conjecture, that OCME intentionally diluted the Duct Tape Swab for the sole purpose of avoiding using HCN. Br. 22. Defendant further criticizes LCN testing, asserting that it is "controversial," no longer used by OCME, and increases stochastic effects, particularly with degraded, touch samples (*see* Br. at 2, 7).

As described in Judge Marrero's decision in *Morgan*, which was based on an "extensive record," including a three-day *Daubert* hearing, "the overwhelming weight of the evidence . . . demonstrates that OCME's LCN testing methodology is firmly rooted in science." *Id.* at 744; *see also id*. at 733 (holding that "the methods of LCN DNA testing that [OCME] employed are sufficiently reliable to satisfy the *Daubert* standard"). In so holding, the Court expressly rejected the same challenges defendant raises with respect to the reliability of LCN. Specifically, Judge Marrero recognized that a small sample size and the use of LCN could increase stochastic effects, but found that OCME's validation studies demonstrated that LCN could produce reliable

results from degraded and touched samples, as well as samples with small quantities of DNA and multiple contributors. *Id.* at 741 ("Each of the three characteristics of the crime scene sample that [defendant] has presented as problematic — the small quantity, the mixed DNA, and the degradation — was tested in OCME's validation studies . . . [and] taken together, they formed the basis for robust and reliable interpretation protocols. . . ."); *see also id.* ("[F]or the casework sample, mixture, and sensitivity studies — over one hundred distinct samples in total — all allelic assignments made were correct.").

The Second Circuit affirmed Judge Marrero's decision. *Morgan*, 675 Fed. App'x at 55-56. And while it "express[ed] no opinion on the propriety of admitting the results of LCN testing in other cases," *id.* at 56, defendant has not identified any reason for reaching a different result here, where OCME used 100 picograms of DNA — more than seven times the amount of DNA present in *Morgan* — and, as described below, the optimal amount for LCN testing.[25] In fact, defendant does not challenge OCME's use of LCN in analyzing the Cellphone Battery Swab, and the Duct Tape Swab should similarly not be excluded.

Contrary to defendant's claim that OCME diluted the Duct Tape Sample for the sole purpose of avoiding HCN testing, in 2007, when the Duct Tape Sample was analyzed, LCN was the preferred method of testing for samples below 150 picograms. *See* O'Connor Decl. at ¶ 13. The reason for this preference was that OCME's validation studies showed that using HCN testing on DNA below 150 picograms increased the risk of allelic drop-out, meaning the risk that true alleles would not be detected. *Id*. LCN, however, was specifically designed for lower amounts of DNA, including that its processes were more sensitive and thus more likely to

[25] The Court further noted that while LCN samples are not put into the FBI's CODIS database, "[t]he publications and testimony the Government has presented demonstrate persuasively that despite dissenting voices, a sufficient scientific underpinning for OCME's LCN methodology exists." *Id.* at 743.

identify and amplify low amounts of DNA. *Id.* As described above, LCN's processes and procedures were also specifically tailored to address the increase of stochastic effects that can arise from amplifying low amounts of DNA. *Id.* Accordingly, OCME's protocols instructed analysts to use LCN for samples with less than 150 picograms. *Id.*; *see also*, O'Connor Decl. Ex. C at 2 (Table 1) (Protocols for High Sensitivity Testing, Version 1.0 (Effective date: January 11, 2006-June 8, 2008)[26] (stating that any sample with a concentration within the range of 4.0 picograms/microliter to 30 picograms/microliter (which translates to 20 to 150 picograms of DNA should use 31 cycles (LCN)).

OCME's validation studies further showed that 100 picograms was the optimal amount of DNA for LCN testing, meaning the amount most likely to produce a reliable result. *See, e.g.*, Ex. C (Theresa Caragine, et al.,) at 252, ("[I]f high amounts of DNA were recovered, extracts were diluted and the target amount of LT-DNA, 100 pg, processed."); *id.* at 253 ("All amplifications were carried out . . . and amplified with the target amount, 100 pg of DNA"); *id.* at 258 ("The optimal amount of DNA, 100 pg . . ."); *see also* O'Connor Decl. at ¶ 11.

Here, because the Duct Tape Swab contained, at most, approximately 121.5 picograms,[27] LCN was an appropriate test to use and OCME analysts properly followed OCME's protocols in selecting LCN testing. Moreover, because OCME's validation studies showed that 100 picograms was the optimal amount of DNA for LCN testing, it was entirely reasonable to dilute the sample to achieve the optimal 100 picogram level. *See* O'Connor Decl. at ¶ 14. Indeed, if OCME analysts had amplified 121.5 picograms of DNA using LCN, it would have created an

[26] Available at: https://www1.nyc.gov/assets/ocme/downloads/pdf/technical-manuals/forensic-biology-technical-manuals/low_copy_dna_011106.pdf.

[27] It is also possible that some amount of DNA could have evaporated during the process such that OCME had less than 121.5 picograms available.

increased risk of technical and biological artifacts. *See* O'Connor Decl. ¶ 10; *see also*, AmpFlister® Identifiler®, PCR Amplification Kit, User Guide, Thermo Fisher Scientific) at 20 (describing negative consequences "[i]f too much DNA is added to the PCR reaction");[28] Bio-Rad, PCR Troubleshooting[29] ("If the template concentration is too high, the polymerase can be inhibited due to carryover of inhibitors or inefficient denaturation.").

D. 97 Allele Cap

Defendant argues that the FST evidence should be excluded because the 97 Allele Cap impacts the likelihood ratio and led to 5 loci being "dropped" in the analysis of the Duct Tape Sample. Br. at 23. As defendant acknowledges, this issue was raised in *Jones*, where 3 alleles were "dropped," and the Court nonetheless denied defendant's *Daubert* motion. *See supra* pp. 20-21 (describing arguments raised in *Jones*); *see also Jones*, 965 F.3d at 157 (describing Dr. Mitchell's testimony on the 97 Allele Cap).

As described above, the 97 Allele Cap was a minor change, which only impacts loci that are of little probative value given that the alleles reflect 97% or more of the population. In addition, the NYS Commission specifically examined and approved FST's use of the 97 Allele Cap. In 2017, a group of lawyers from the Legal Aid Society and Federal Defenders of New York filed a written complaint with the New York State Inspector General ("IG"), which raised concerns about FST, including a concern about the 97 Allele Cap. The IG referred the matter to the NYS Commission, which in turn referred the matter to the DNA Subcommittee. The DNA Subcommittee investigated the allegations, and in a letter dated December 4, 2017, soundly rejected them and reaffirmed its approval of FST. Specifically, the DNA Subcommittee found

[28] Available at: https://assets.thermofisher.com/TFS-Assets/LSG/manuals/cms_041201.pdf.

[29] Available at: https://www.bio-rad.com/en-us/applications-technologies/pcr-troubleshooting?ID=LUSO3HC4S#gel3.

"that there was no 'significant malfunction,'" as was alleged. *Jones* Doc. 302, Ex. A.

Accordingly, as confirmed by OCME's performance checks, which were reviewed and expressly endorsed by the DNA Subcommittee, FST continues to produce reliable results with the 97 Allele Cap. *See id.* at 3 ("[T]he DNA Subcommittee does not believe that any re-validation was required as the performance checks were sufficient."). As the Second Circuit has explained, "a slight modification of an otherwise reliable method will not render an expert's opinion per se inadmissible," but rather evidence should be excluded only when the "flaw is large enough that the expert lacks good grounds for his or her conclusion." *Amorgianos v. National R.R. Passenger Corp.*, 303 F.3d 256, 267 (2d Cir. 2002).

If anything, the use of the 97 Allele Cap in this case likely benefited the defendant. The Duct Tape Swab had 5 loci where alleles reflected 97% or more of the overall population. Because Cortorreal's alleles were present in each of these 5 loci, absent the 97 Allele Cap, the likelihood ratio for each locus would likely have been greater than 1, but here, due to the 97 Allele Cap, a likelihood ratio of 1 was assigned.

Defendant's reliance on a 2019 presentation and paper do not support reaching a different conclusion from *Jones*.[30] First, defendant relies on a presentation and corresponding conference paper, which is posted online, not published in any peer-reviewed journal. *See* Ex. K (hereinafter the "Matthews Article"). In the Matthews Article, the authors describe how they ran FST with and without the 97 Allele Cap and identified changes in the likelihood ratios. *See* at 325. However, the differences were minimal. For example, of the 1,245 tests run for known contributors, the verbal equivalence changed in only 36 (2.9%) tests. Not only was this a

[30] The materials are described in Adams' Declaration pages 31-32. As described above, the Government has serious concerns about Adams' qualifications as an expert on topics relating to forensic DNA testing.

relatively small change, but many changes involved *reducing* the likelihood ratio, which as described above, is the generally expected result for true contributors, whose alleles would necessarily be present in all affected loci.[31] Such a finding further supports that, if anything, the 97 Allele Cap likely reduced the likelihood ratio in this case given that Corttorreal's alleles were present in all of the impacted loci. [32]

In testing non-contributors *i.e.*, testing for false positives, the Matthews Article found that the change was minuscule and effectively netted out. Specifically, the article claims that in 28,000 comparisons, only 5 results changed to false inclusions, while 4 changed to true exclusions. The study claims that this supports that the false positive rate of FST is thus 0.08%,[33] as opposed to 0.03% — a change which plainly does not undermine the Second Circuit's affirmation of FST. Moreover, in practice, the false positive rate of FST is likely even lower because FST is not run unless an OCME analyst first determines that a suspect could be a contributor. Accordingly, many of the samples run in the non-contributor test would likely never have been run in practice. *See also id.* (including a chart identifying changes in verbal

[31] Given that this study involved only known contributors, it did not assess the extent to which the 97 Allele Cap introduced false positives. As described in the following paragraph, the study testing false positives demonstrated that the 97 Allele Cap had effectively a net-zero impact.

[32] Defendant claims that 23.7% of the two- and three-person mixtures considered in FST's validation study "ultimately exhibited traits that OCME retroactively determined to be undesirable." Br. 29 and Adams Decl. at 31. This appears to be a reference to the fact that the Matthews presentation found that approximately 23.7% of the samples from OCME's known contributors' study would have triggered the 97 Allele Cap. However, as the presentation concludes, using the 97 Allele Cap on these samples created minimal changes to the likelihood ratios. *See* Matthews Presentation at 325.

[33] It is further unclear from the article whether this percentage was correctly calculated and is an appropriate comparison to the 0.03% false positive rate calculated in FST's validation studies. Whereas FST's false positive rate was based on more than half a million tests, the article claims to have calculated its false positive rate from 28,000 comparisons.

equivalence from OCME's validation study and concluding that the changes were "modest").

The defendant further relies on a 2019 study, which found that, on average, where the 97 Allele Cap changes the likelihood ratio, it becomes lower if applied to loci with six alleles, and higher if applied to loci with five alleles.[34] Defendant argues because three of the impacted loci from the Duct Tape Swab had five alleles, the likelihood ratio was improperly increased. Br. 24-25. However, the article explains that it's finding was just an average and that there were many examples where the likelihood ratio decreased when applied to loci with five alleles. *See* Gasston Article at 3 (including graphs showing changes both above and below 1 for five and six alleles). The article further acknowledges that the ultimate impact depends on a range of factors, and that many of the tests may not have been run in practice, given that OCME analysts manually exclude samples where the suspect's profile does not match the sample. *Id.* at 4.

If anything, these studies support the ongoing validity of FST. They demonstrate that with the use of FST's publicly available source code, researchers can and have independently assessed FST's operation, including the impact of the 97 Allele Cap, and have not identified significant issues. As discussed throughout, FST underwent an extensive testing, validation, review, re-review (specifically focusing on the 97 Allele Cap), and accreditation process. A modest change to the source code — which likely benefited the defendant in this case — does not render it inadmissible.

E. Inapplicability of Computer Science Standards

Finally, relying on Adams' Declaration, defendant repeats the same arguments raised and rejected in *Jones* that FST "does not comport with common software engineering standards." Br.

[34] *See* Julia Gasston, *et al.*, "An Examination of Aspects of the Probabilistic Genotyping Tool: Forensic Statistical Tool," (2019) WIREs Forensic Sci. 2(3): 1-6. Available at: https://wires.onlinelibrary.wiley.com/doi/epdf/10.1002/wfs2.1362 (hereinafter "Gasston Article").

at 26.[35] Ultimately, defendant cannot point to a single coding issue that renders FST unreliable, or any regulator or organization in the forensic science field that requires systems like FST to comply with computer science standards. *See* O'Connor Decl. at ¶ 15 and Exs. D-F (involving industry guidelines, none of which require conforming to computer science standards).

Defendant claims that "[t]he public still does precisely not know what OCME intended FST, the software, to accomplish," and complains that OCME has not produced specifications or software requirements that it used to instruct outside contractors. Br. at 26. However, FST's source code has been publicly available for years, which as demonstrated by the Matthews and Gasston Articles defendant cites, has allowed researchers to assess how the program operates. In addition, as Dr. Mitchell, one of the developers of FST, testified at the *Jones* hearing, FST was designed to compute a likelihood ratio that was not possible to compute by hand in real time. Accordingly, her goal was that the math be calculated correctly, which she was able to confirm through manual confirmations and validation studies. *See Jones* Tr. 169-70.

Defendant's repeated claim that there is no way to test whether FST accomplishes its objectives is inconsistent with FST's validation studies, which demonstrate that FST accomplishes what it was intended to accomplish — reliably calculate likelihood ratios. Defendant's attempts to impose software standards to the field of forensic DNA analysis is not the proper basis for a *Daubert* motion. Indeed, Adams' testimony in *Jones* demonstrates that his arguments are not at all established in the field of probabilistic genotyping programs like FST. *See* Ex. B (*Jones* Tr.) at 717 (testifying that despite asking for the documentation in all cases he reviews, "[i]n no probabilistic genotyping system have I ever received" the software standard

[35] As described above, Adams testified about these concerns at length in *Jones*. Although the *Jones* decision did not reference them explicitly, it nonetheless did not find it a reason to exclude the evidence and accordingly rejected defendant's motion.

documents he claims FST should have).

CONCLUSION

For the foregoing reasons, the Government respectfully requests that the Court deny the Motion to Preclude Evidence Produced by the Forensic Statistical Tool without holding a hearing.

Dated: New York, New York
September 7, 2021

Respectfully submitted,

AUDREY STRAUSS
United States Attorney for the
Southern District of New York

By: /s/
Courtney L. Heavey
Adam Hobson
Justin Rodriguez
Assistant United States Attorneys
(914) 993-1927 / 212-637-2484/2591